

REMARKS

In Paper 24 the examiner stated that the reply filed on April 14, 2003 (Paper 23) is not fully responsive to the prior office action because applicants have not defined the species in the elected group. Applicants had elected with traverse SuperGroup F, Group I and SEQ ID NOs: 1 and 2. The examiner stated that the nature of SEQ ID NOs: 16, 19, 20, 21, and 22 remain unclear. These sequences have been deleted from the new sequence listing. Previous SEQ ID NOs: 17, 18, 25 and 28 have been retained as they are not duplicate sequences. They have been renumbered as SEQ ID NOs: 16-19. Therefore, applicants believe the examiner's objection now is moot.

It is believed that by submitting the present amendment and sequence listing diskette, the application now fully complies with the requirements of 37 CFR 1.821-1.825. Favorable action by the examiner is solicited.

**A check in the amount of \$110.00 is attached to cover the required one month extension fee.**

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11.0345. Please credit any excess fees to such deposit account.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

TECH CENTER 1600/2900

IN THE SPECIFICATION

Delete the sequence listing of the specification and substitute replacement  
pages 1-25 attached hereto as separate pages.

Amend the paragraphs from page 35, line 25 through page 37, line 15, as  
follows:

~~SEQ ID NO. 16: The amino acid sequence of the yeast ORF YNR008w from  
*Saccharomyces cerevisiae*.~~

SEQ ID NO. ~~17~~ 16: Amino acid sequence of the region of the *Arabidopsis thaliana*  
genomic sequence (AC004557).

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SEQ ID NO. ~~18~~ 17: Amino acid sequence of the region of the *Arabidopsis thaliana*  
genomic sequence (AB006704).

~~SEQ ID NO. 19: The corresponding genomic DNA sequence and amino acid sequence  
of the yeast ORF YNR008w from *Saccharomyces cerevisiae*.~~

~~SEQ ID NO. 20: The amino acid sequence of the yeast ORF YNR008w from  
*Saccharomyces cerevisiae* derived from the corresponding genomic DNA sequence.~~

~~SEQ ID NO. 21: Genomic DNA sequence of the *Saccharomyces cerevisiae* PDAT  
gene, YNR008w, genebank nucleotide ID number 1302481, and the suggested  
YNR008w amino acid sequence.~~

~~SEQ ID NO. 22: The suggested amino acid sequence of the yeast gene YNR008w~~

from *Saccharomyces cerevisiae*.

~~SEQ ID NO. 23: Genomic DNA sequence of the *Schizosaccharomyces pombe* gene SPBG776.14.~~

~~SEQ ID NO. 24: Genomic DNA sequence of a part of the *Arabidopsis thaliana* locus with genebank accession number AB006704.~~

SEQ ID NO. 25 18: Nucleotide sequence and the corresponding amino acid sequence of the *Arabidopsis thaliana* EST-clone with genebank accession number T04806, and ID number 315966.

~~SEQ ID NO. 26: Nucleotide and amino acid sequence of the *Zea mays* cDNA clone with genebank ID number g4388167.~~

32 ~~SEQ ID NO. 7b: Amino acid sequence of the *Zea mays* cDNA clone with genebank ID number g4388167.~~

~~SEQ ID NO. 8b 19: DNA sequence of part of the *Neurospora crassa* cDNA clone WO7G1, ID number g4241729.~~

~~SEQ ID NO. 9b: Genomic DNA sequence of part of the *Arabidopsis thaliana* locus with genebank accession number AC004557.~~

~~SEQ ID NO. 10b: Genomic DNA sequence of part of the *Arabidopsis thaliana* locus with genebank accession number AC003027.~~

~~SEQ ID NO. 11b: DNA sequence of part of the *Lycopersicon esculentum* cDNA clone with genebank accession number A1486635.~~

Page 4, delete the previously added first paragraph as follows:

~~The instant invention pertains further to an enzyme comprising an amino acid sequence as set forth in SEQ ID NO. 16, 22 or 20 or a functional fragment, derivative, allele, homologue or isoenzyme thereof.~~

Amend the paragraph (for the second time) on page 4, lines 13-27, as follows:

13  
Also, partially sequenced cDNA clone from Neurospora crassa (SEQ ID NO. 9) and a Zea mays EST (Extended Sequence Tag) clone (SEQ ID NO. 7) and corresponding putative amino acid sequence (SEQ ID NO. 8) were identified. Finally, two cDNA clones were identified, one Arabidopsis thaliana EST (SEQ ID NO. 5 and corresponding predicted amino acid sequence SEQ ID NO. 6) and a Lycopersicon esculentum EST clone (SEQ ID NO. 12) were identified. Further, enzymes designated as PDAT comprising an amino acid sequence selected from the group consisting of sequences as set forth in SEQ ID NO. ~~47, 18, 25, 6 or 27~~ 16, 17 and 18 are contemplated within the scope of the invention. Moreover, an enzyme comprising an amino acid sequence encoded through a nucleotide sequence, a portion, derivative, allele or homologue thereof selected from the group consisting of sequences as set forth in SEQ ID NO. ~~21, 3, 23, 4, 19, 24, 5, 25, 26, 7, 28, 9, 29, 10, 30, 11, 31 or 12~~ 1, 3, 4, 5, 7, 9, 10, 11, 12, 18 or 19 or a functional fragment, derivative, allele, homologue or isoenzyme of the enzyme encoding amino acid sequence are included within the scope of the invention.

Amend the paragraph (for the second time) on page 7, lines 1-11, as follows:

34 Further included is a nucleotide sequence selected from the group consisting of sequences set forth in SEQ ID NO. ~~21, 3, 23, 4, 19, 26, 29, 10, 30 or 11~~ 1, 3, 4, 10 or 11 or a portion, derivative, allele or homologue thereof. The invention pertains a partial nucleotide sequence corresponding to a fulllength nucleotide sequence selected from the group consisting of sequences set forth in SEQ ID NO. ~~5, 25, 26, 7, 28, 9, 31 or 12~~ 5, 7, 9, 12, 18 or 19 or a portion, derivative, allele or homologue thereof. Moreover, a nucleotide sequence comprising a nucleotide sequence which is at least 40% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID NO. ~~1, 21, 3, 23, 4, 19, 24, 5, 25, 26, 7, 28, 9, 29, 10, 30, 11, 31 or 12~~ 1, 3, 4, 5, 7, 9, 10, 11, 12, 18 or 19 is contemplated within the scope of the invention.

Amend the paragraph (for the second time) on page 21, lines 17-26, as follows:

35 *PDAT genes.* Nucleotide and amino acid sequences of several PDAT genes are given as SEQ ID NO. 1 through 15. Further provisional and/or partial sequences are given as SEQ ID NO. 16 through 19 ~~20 and 21 through 31~~, respectively. One of the Arabidopsis genomic sequences (SEQ ID NO. 4) identified an Arabidopsis EST cDNA clone; T04806. This cDNA clone was fully characterized and the nucleotide sequence is given as SEQ ID NO. 5. Based on the sequence homology of the T04806 cDNA and the *Arabidopsis thaliana* genomic DNA sequence (SEQ ID NO. 4) it is apparent that an

35 additional A is present at position 417 in the cDNA clone (data not shown). Excluding this nucleotide would give the amino acid sequence depicted in SEQ ID NO. 12.

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**IN THE CLAIMS**

✓ Cancel claim 4.

Amend claims 5, 6, 9-11 and 16, and add new claims 33-34, as follows:

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5. (currently amended) An enzyme according to claim 1, comprising an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NO: 6, 8, 13, 14, 15, 16, 17, and 18 ~~17, 18, 25, 6, 27, 8, 13, 14, 15~~ or a functional fragment, derivative, allele, ~~homologue or isoenzyme~~ homolog or isozyme thereof.

36 6. (currently amended) An enzyme according to claim 1, comprising an amino acid sequence encoded through a nucleotide sequence, a portion, derivative, allele or ~~homologue~~ homolog thereof selected from the group consisting of sequences set forth in SEQ ID NO. ~~1, 21, 3, 23, 4, 19, 26, 5, 25, 26, 7, 28, 9, 29, 10, 30, 11, 31, 42,~~ 1, 3, 4, 5, 7, 9, 10, 11, 12, 18, 19 or a functional fragment, derivative, allele, ~~homologue or isoenzyme~~ homolog or isozyme of the enzyme encoding amino acid sequence.

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37 9. (currently amended) A nucleotide sequence according to claim 7, selected from the group consisting of sequences as set forth in SEQ ID NO. ~~1, 21, 3, 23, 4, 19, 24, 29, 10, 30~~ 3, 4, 10, or 11 or a portion, derivative, allele or ~~homologue~~ thereof.

10. (currently amended) A partial nucleotide sequence corresponding to a fulllength nucleotide sequence according to claim 7, selected from the group consisting of sequences as set forth in SEQ ID NO. ~~5, 25, 26, 7, 28, 9, 31, or 12~~ 5, 7, 9, 12, 18, 19 or a portion, derivative, allele or homologue thereof.

37 11. (currently amended) A nucleotide sequence according to claim 7, comprising a nucleotide sequence which is at least 40% homologous to a nucleotide sequence selected from the group consisting of those sequences as set forth in SEQ ID NO. ~~21, 3, 23, 4, 19, 24, 5, 25, 26, 7, 28, 9, 29, 10, 30, 11, 31 or 12~~ 1, 3, 4, 5, 7, 9, 10, 11, 12, 18, or 19.

38 16. (currently amended) A transgenic cell or organism containing a nucleotide sequence according to claim 7 ~~and/or a gene construct according to claim 12 and/or a vector according to claims 13-28.~~

34 33. (new) A transgenic cell or organism containing a gene construct according to claim 12.

35 34. (new) A transgenic cell or organism containing a vector according to claim 28.